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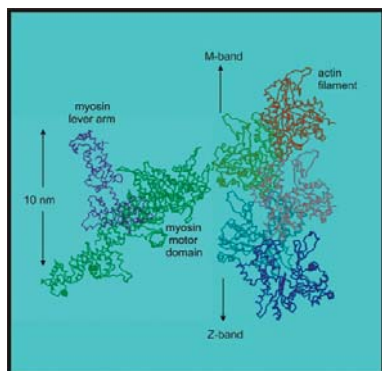
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Low-angle X-ray fibre diffraction can be used to determine protein sub-domain positions to very high precision. The approach outlined in AL-Khayat *et al.* (this volume) shows how simulated-annealing parameter searches, using the CCP13 program MOVIE, of myosin cross-bridges in relaxed insect flight muscle against observed X-ray diffraction data have led to the first *in situ* atomic model of the pre-powerstroke conformation for the myosin head. This turned out to be remarkably comparable to a crystallographically-determined structure for a similar head conformation of truncated vertebrate smooth muscle myosin solved using molecular replacement methodology by Dominguez *et al.* (1998: *Cell* 94, 559-571). The transition from the head shape in relaxed insect muscle to the different head shape in rigor may be revealing the working stroke of the myosin head involved in muscle contraction and force generation.

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